

In the Specification

Page 10, line 3, change "PTA-325" to --PTA-326--.

In the Claims

45. (Twice Amended) A method of compiling a positive sense functional gene profile of an organism comprising:

(a) preparing a library of [cDNAs, genomic DNAs, or a pool of RNAs] DNA or RNA sequences from a non-plant donor organism, and constructing recombinant viral nucleic acids comprising [a] an unidentified nucleic acid insert [derived] obtained from said library in a positive sense orientation;

(b) infecting a plant host with one [of] or more said recombinant viral nucleic acids;

(c) transiently expressing the unidentified nucleic acid [in a positive sense orientation] in said plant host;

(d) determining one or more phenotypic or biochemical changes in said plant host;

(e) identifying a trait associated with [a] said one or more phenotypic or biochemical changes;

(f) identifying [a donor gene or a plant host gene, which is associated with the trait; and] said recombinant viral nucleic acid that results in said one or more changes in said plant host;

(g) repeating steps (b)-(f) until at least one [donor organism gene or one plant host

gene] nucleic acid associated with said trait is identified, whereby a positive sense functional gene profile of said plant host or said donor organism is compiled.

Add the following new claims 46-59:

57-46. (New) A method of compiling a positive sense functional gene profile of an organism comprising:

a) preparing a library of DNA or RNA sequences from a non-plant donor

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organism, and constructing recombinant viral nucleic acids comprising an unidentified nucleic acid insert obtained from said library;

- b) infecting a plant host with one or more said recombinant viral nucleic acids;
- c) transiently expressing said recombinant nucleic acid in the plant host;
- d) determining one or more changes in phenotypic or biochemical changes in the plant host;
- e) identifying a trait associated with said one or more phenotypic or biochemical changes;
- f) identifying the recombinant viral nucleic acid that results in said one or more changes in the plant host;
- g) determining and selecting the sequence of said nucleic acid insert in said recombinant viral nucleic acid that is in a positive sense orientation; and
- h) repeating steps b)-g) until at least one nucleic acid associated with said trait is identified, whereby a positive functional gene profile of the plant host or the donor plant is compiled.

57. (New) The method according to Claim 45 or 46, further comprising a step of identifying a donor gene associated with said trait.

58. (New) The method according to Claim 45 or 46, further comprising a step of identifying a host plant gene associated with said trait.

59. (New) The method according to Claim 45, wherein said plant host is *Nicotiana*.

56. (New) The method according to Claim 49, wherein said plant host is *Nicotiana benthamina* or *Nicotiana cleavlandii*.

51. (New) The method according to Claim 45, wherein a positive sense RNA is produced in the cytoplasm of said plant host, and said positive sense RNAs results in a reduced or enhanced expression of an endogenous gene in said plant host.

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52. (New) The method according to Claim 45, wherein a positive sense RNA is produced in the cytoplasm of said host plant, and said positive sense RNA results in overexpression of a protein in said host plant.

53. (New) The method according to Claim 45, wherein said recombinant viral nucleic acid further comprises a native plant viral subgenomic promoter and a plant viral coat protein coding sequence.

54. (New) The method according to Claim 53, wherein said recombinant viral nucleic acid further comprises a non-native plant viral subgenomic promoter, said native plant viral subgenomic promoter initiates transcription of said plant viral coat protein sequence and said non-native plant viral subgenomic promoter initiates transcription of said nucleic acid sequence.

55. (New) The method according to Claim 45, wherein said recombinant viral nucleic acids are obtained from a plant virus.

56. (New) The method according to Claim 55, wherein said plant virus is a single-stranded plus sense RNA virus.

57. (New) The method according to Claim 56, wherein said plant virus is selected from the group consisting of a potyvirus, a tobamovirus, and a bromovirus..

58. (New) The method according to Claim 57, wherein said tobamovirus is a tobacco mosaic virus.

59. (New) The method according to Claim 57, wherein said potyvirus is a rice necrosis virus--.

#### REMARKS

##### The Amendments

The title of the application is amended to reflect the elected claims.

Page 10, the typographical error of the ATCC No. of pBS 740 AT #855 is corrected.